



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179285

TO: Chun Crowder
Location: REM-3B59/3C70
Art Unit: 1644
Thursday, February 16, 2006
Case Serial Number: 10/524134

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Crowder,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

Handwritten text, possibly a signature or date, oriented vertically.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:53:06 ; Search time 10.3246 Seconds
(without alignments)
147.285 Million cell updates/sec

Title: US-10-524-134-4

Sequence: 1 DILITOSPALISVSPGERVS.....CQGSNTWPTFGGTGKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 1421169 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	US-11-108-135-26	Sequence 26, App1
2	557	100.0	107	US-11-126-978-26	Sequence 26, App1
3	499	89.6	107	US-11-004-590-234	Sequence 234, App1
4	484	86.9	107	US-11-010-954-3	Sequence 3, App1
5	484	86.9	107	US-11-053-750-3	Sequence 3, App1
6	484	86.9	107	US-11-053-749-3	Sequence 3, App1
7	484	86.9	107	US-11-170-753-3	Sequence 3, App1
8	484	86.9	107	US-11-179-359-3	Sequence 3, App1
9	484	86.9	107	US-11-181-030-3	Sequence 3, App1
10	484	86.9	107	US-11-182-033-3	Sequence 3, App1
11	484	86.9	107	US-11-195-589-3	Sequence 3, App1
12	484	86.9	109	US-11-005-726-10	Sequence 10, App1
13	484	86.9	117	US-11-005-726-12	Sequence 12, App1
14	484	86.9	214	US-11-005-726-163	Sequence 163, App1
15	484	86.9	226	US-11-183-205-42	Sequence 42, App1
16	447	80.3	108	US-11-003-726-7	Sequence 7, App1
17	445	79.9	107	US-11-108-135-18	Sequence 18, App1
18	445	79.9	107	US-11-126-978-18	Sequence 18, App1
19	440	79.0	107	US-11-004-590-379	Sequence 379, App1
20	437	78.5	107	US-11-108-135-30	Sequence 251, App1
21	437	78.5	107	US-11-004-590-251	Sequence 251, App1
22	437	78.5	107	US-11-004-590-259	Sequence 259, App1
23	437	78.5	107	US-11-004-590-324	Sequence 324, App1
24	437	78.5	107	US-11-004-590-381	Sequence 381, App1
25	437	78.5	107	US-11-126-978-20	Sequence 20, App1

26	436	78.3	107	US-11-004-590-250	Sequence 250, App1
27	436	78.3	107	US-11-004-590-257	Sequence 257, App1
28	436	78.3	107	US-11-004-590-260	Sequence 260, App1
29	436	78.3	107	US-11-004-590-323	Sequence 323, App1
30	435	78.1	107	US-11-004-590-248	Sequence 248, App1
31	435	78.1	107	US-11-004-590-255	Sequence 255, App1
32	435	78.1	108	US-11-005-726-5	Sequence 5, App1
33	434	77.9	107	US-11-004-590-246	Sequence 246, App1
34	433	77.7	107	US-11-108-135-22	Sequence 22, App1
35	433	77.7	107	US-11-004-590-325	Sequence 325, App1
36	433	77.7	107	US-11-004-590-325	Sequence 325, App1
37	433	77.7	107	US-11-126-978-22	Sequence 22, App1
38	432	77.6	107	US-11-004-590-249	Sequence 249, App1
39	432	77.6	107	US-11-004-590-254	Sequence 254, App1
40	432	77.6	107	US-11-004-590-282	Sequence 282, App1
41	432	77.6	107	US-11-004-590-312	Sequence 312, App1
42	432	77.6	108	US-11-005-726-8	Sequence 8, App1
43	431	77.4	107	US-11-004-590-245	Sequence 245, App1
44	431	77.4	107	US-11-004-590-293	Sequence 293, App1
45	431	77.4	107	US-11-004-590-303	Sequence 303, App1

ALIGNMENTS

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RESULT 1
US-11-108-135-26
Sequence 26, Application US/11108135
Publication No. US20050260213A1
GENERAL INFORMATION:
APPLICANT: Koenig, Scott
APPLICANT: Veri, Maria Concetta
APPLICANT: Tuallion, Nadine
APPLICANT: Bonvin, Ezio
APPLICANT: Stavenhagen, Jeffrey
APPLICANT: Rankin, Christopher
TITLE OR INVENTION: FC-gamma-RIIb-specific antibodies and methods of use thereof
FILE REFERENCE: 11183-018-999
CURRENT APPLICATION NUMBER: US/11/108,135
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/562,804
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/582,044
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/582,045
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/654,713
PRIOR FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 107
TYPE: PRT
ORGANISM: mus sp.
FEATURE:
OTHER INFORMATION: Mouse 286 light chain variable region
US-11-108-135-26
Query Match 100.0%; Score 557; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.2e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DILITOSPALISVSPGERVSFSCRTSGTGNHMYOQRTNGPFRLLIKVSEISIGIPS 60
Db 1 DILITOSPALISVSPGERVSFSCRTSGTGNHMYOQRTNGPFRLLIKVSEISIGIPS 60
OY 61 RFSGSGGTDFILINSVESEDIADYYCQGSNTWPTFGGTGKLEIK 107
Db 61 RFSGSGGTDFILINSVESEDIADYYCQGSNTWPTFGGTGKLEIK 107
RESULT 2
US-11-126-978-26
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Sequence 26, Application US/1126978
Publication No. US20060013810A1
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie Sydnor
APPLICANT: Huang, Ling
TITLE OF INVENTION: HUMANIZED FCgammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THEREIN
FILE REFERENCE: 11183-018-999
CURRENT APPLICATION NUMBER: US/11/126,978
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: 60/582,043
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: 60/569,882
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 107
TYPE: PRT
ORGANISM: mus sp.
FEATURE:
OTHER INFORMATION: Mouse 2B6 light chain variable region
US-11-126-978-26
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Query Match 100.0%; Score 557; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 8,2e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 DILLTQSPAILSVSGRVSFSCRTSOSIGTNIHWYQORTNGPRLLIKVSSEISGIPS 60
Db 1 DILLTQSPAILSVSGRVSFSCRTSOSIGTNIHWYQORTNGPRLLIKVSSEISGIPS 60
Qy 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
Db 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
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RESULT 3
US-11-004-590-234
Sequence 234, Application US/11004590
Publication No. US20060008883A1
GENERAL INFORMATION:
APPLICANT: Lazari, Gregory Alan
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
FILE REFERENCE: 185832/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US 60/619,483
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patencin version 3.3
SEQ ID NO 234
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-004-590-234
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Best Local Similarity 89.7%; Pred. No. 3,8e-34;
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Db 1 DILLTQSPAILSVSGRVSFSCRTSOSIGTNIHWYQORTNGPRLLIKVSSEISGIPS 60
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Qy 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
Db 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
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RESULT 4
US-11-010-954-3
Sequence 3, Application US/11010954
Publication No. US20050249735A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilecek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghayeb, John
APPLICANT: Knight, David
APPLICANT: Siegel, Scott
APPLICANT: Shealy, David
TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antib
FILE REFERENCE: 0975.1005-043
CURRENT APPLICATION NUMBER: US/11/010,954
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US 10/637,759
PRIOR FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US 09/920,137
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 09/927,703
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 60/236,826
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/223,360
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 107
TYPE: PRT
ORGANISM: Mus Balb/c
US-11-010-954-3
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Query Match 86.9%; Score 484; DB 7; Length 107;
Best Local Similarity 85.0%; Pred. No. 6e-33;
Matches 91; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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Qy 1 DILLTQSPAILSVSGRVSFSCRTSOSIGTNIHWYQORTNGPRLLIKVSSEISGIPS 60
Db 1 DILLTQSPAILSVSGRVSFSCRTSOSIGTNIHWYQORTNGPRLLIKVSSEISGIPS 60
Qy 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
Db 61 RFGSGSGTDFLTLSINVSSESDIADYCCQGSNTWPTFTGGGKLEIK 107
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RESULT 5
US-11-053-750-3
Sequence 3, Application US/11053750
Publication No. US20050255104A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilecek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghayeb, John
APPLICANT: Knight, David
APPLICANT: Siegel, Scott
APPLICANT: Scallion, Bernard
TITLE OF INVENTION: Methods of Treating Psoriasis Using
FILE REFERENCE: 0975.1005-045
CURRENT APPLICATION NUMBER: US/11/053,750
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: U.S. 09/927,703
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:52:22 ; Search time 106.061 Seconds
(without alignments)
421.527 Million cell updates/sec

Title: US-10-524-134-4

Sequence: 1 DILITOSPALISVSGRVS.....COGSNTWPTFGGCKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	100.0	107	4	US-10-643-857-4
2	557	100.0	107	5	US-10-524-134-4
3	504	90.5	107	5	US-10-923-068-507
4	504	90.5	108	4	US-10-412-703A-129
5	503	90.3	107	3	US-09-842-776A-58
6	503	90.3	107	4	US-10-467-546-1
7	503	90.3	107	6	US-10-666-332-1
8	503	90.3	107	6	US-11-050-435-32
9	503	90.3	111	6	US-11-050-435-6
10	503	90.3	214	4	US-10-467-546-3
11	503	90.3	214	5	US-10-666-332-3
12	500	89.8	107	4	US-10-239-656-38
13	500	89.8	510	4	US-10-239-656-49
14	499	89.6	107	4	US-10-308-817-129
15	499	89.6	107	4	US-10-453-698-129
16	499	89.6	107	6	US-11-004-054-2
17	499	89.6	127	4	US-10-374-600-5
18	499	89.6	127	4	US-10-374-600-11
19	499	89.6	127	4	US-10-374-600-15
20	499	89.6	127	4	US-10-374-531-5
21	499	89.6	127	4	US-10-374-531-11
22	499	89.6	127	4	US-10-374-531-15
23	499	89.6	236	5	US-10-728-723-18
24	498	89.4	107	5	US-10-901-736-1
25	498	89.4	242	4	US-10-336-210-9
26	498	89.4	244	3	US-09-940-391-1
27	498	89.4	244	4	US-10-336-210-8

28	497	89.2	107	4	US-10-239-656-28	Sequence 28, Appl
29	497	89.2	510	4	US-10-239-656-48	Sequence 48, Appl
30	496	89.0	107	4	US-10-308-817-130	Sequence 130, App
31	496	89.0	107	4	US-10-453-698-130	Sequence 130, App
32	489	87.8	214	5	US-10-488-074-72	Sequence 72, Appl
33	489	87.8	214	5	US-10-488-074-68	Sequence 68, Appl
34	484	86.9	107	3	US-09-756-301A-3	Sequence 3, Appl
35	484	86.9	107	3	US-09-927-703-3	Sequence 3, Appl
36	484	86.9	107	3	US-09-766-535A-3	Sequence 3, Appl
37	484	86.9	107	3	US-09-756-161A-3	Sequence 3, Appl
38	484	86.9	107	3	US-09-756-398B-3	Sequence 3, Appl
39	484	86.9	107	3	US-09-897-724-3	Sequence 3, Appl
40	484	86.9	107	4	US-10-010-229-3	Sequence 3, Appl
41	484	86.9	107	4	US-10-043-450-3	Sequence 3, Appl
42	484	86.9	107	4	US-10-044-534-3	Sequence 3, Appl
43	484	86.9	107	4	US-10-043-432-3	Sequence 3, Appl
44	484	86.9	107	4	US-10-208-145-3	Sequence 3, Appl
45	484	86.9	107	4	US-10-198-845-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-10-643-857-4
Sequence 4, Application US/10643857
Publication No. US20040185045A1
GENERAL INFORMATION:
APPLICANT: Verig, Maria Conceita
TITLE OF INVENTION: Anti-FcGR1B monoclonal antibodies and their use in enhancing
FILE REFERENCE: 11183-010-999
CURRENT APPLICATION NUMBER: US/10/643,857
CURRENT FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: 60/403,266
PRIOR FILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-643-857-4

Query Match 100.0%; Score 557; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DILITOSPALISVSGRVSFSCRTSOSIGTNIHWYQORTNGFPRLLIKNVSEISIGIPS 60
Db 1 DILITOSPALISVSGRVSFSCRTSOSIGTNIHWYQORTNGFPRLLIKNVSEISIGIPS 60

Cy 61 RFGSGSGTDFILINSVSESDIADYYCOGSNTWPTFGGCKLEIK 107
Db 61 RFGSGSGTDFILINSVSESDIADYYCOGSNTWPTFGGCKLEIK 107

RESULT 2
US-10-524-134-4
Sequence 4, Application US/10524134
Publication No. US20050215767A1
GENERAL INFORMATION:
APPLICANT: Koenig, Scott
TITLE OF INVENTION: Anti-FcGR1B monoclonal antibodies and their use in enhancing
FILE REFERENCE: 11183-003-999
CURRENT APPLICATION NUMBER: US/10/524,134
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: PCT/US03/25399
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: 60/403,266
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; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-524-134-4

Query Match          100.0%; Score 557; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60
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DB 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60

QY 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107
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DB 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107

RESULT 3
US-10-923-068-507
; Sequence 507, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dai, Acqua, William
; APPLICANT: Damachroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: A6600US
; CURRENT APPLICATION NUMBER: US/10/923, 068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 507
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-923-068-507

Query Match          90.5%; Score 504; DB 5; Length 107;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
Matches 97; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60
   |||||
DB 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60

QY 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107
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DB 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107

RESULT 4
US-10-412-703A-129
; Sequence 129, Application US/10412703A
; Publication No. US20030219439A1
; GENERAL INFORMATION:
; APPLICANT: Reed et al.
; TITLE OF INVENTION: Recombinant Anti-Interleukin-9 Antibodies
; FILE REFERENCE: IL400US
; CURRENT APPLICATION NUMBER: US/10/412, 703A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371, 728
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/371, 683
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 108
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-703A-129

Query Match          90.5%; Score 504; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 2.3e-41;
Matches 97; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60
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DB 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60

QY 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107
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DB 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107

RESULT 5
US-09-842-776A-58
; Sequence 58, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842, 776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-842-776A-58

Query Match          90.3%; Score 503; DB 3; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.9e-41;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60
   |||||
DB 1 DILLTQSPALLSVSPGERVSFSCRTSOSIGTNIMHYQOQRTNGFPRLLIKVNSESISGIPS 60

QY 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107
   |||||
DB 61 RFSGSGSGTDFLTLSINSVSESDIADYYCQOQNTWPFTEGGGTKEIK 107

RESULT 6
US-10-467-546-1
; Sequence 1, Application US/10467546
; Publication No. US20040096901A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andrae Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: PCT/EP02/01420
; CURRENT APPLICATION NUMBER: US/10/467, 546
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:36:50 ; Search time 30.9737 Seconds

(without alignments)
285.607 Million cell updates/sec

Title: US-10-524-134-4

Perfect score: 557
Sequence: 1 DILLTQSPALISVPSGRVS.....CQGSNTWPTFGSTKLEIK 107Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	89.4	107	1	US-08-476-176B-4
2	498	89.4	107	2	US-08-127-721A-4
3	498	89.4	107	2	US-08-485-246A-4
4	498	89.4	244	2	US-09-244-369B-1
5	498	89.4	244	2	US-09-940-391-1
6	494	88.7	240	1	US-07-956-399-2
7	492	88.3	107	1	US-08-233-081B-40
8	491	88.2	239	1	US-07-956-399-4
9	487	87.4	106	1	US-08-800-198-4
10	487	87.4	106	2	US-09-296-595-4
11	487	87.4	240	1	US-08-800-198-8
12	487	87.4	240	2	US-09-296-595-8
13	484	86.9	107	1	US-08-192-102-3
14	484	86.9	107	1	US-08-324-799-3
15	484	86.9	107	1	US-08-192-661A-3
16	484	86.9	107	2	US-09-133-119-3
17	484	86.9	107	2	US-08-192-093A-3
18	484	86.9	107	2	US-09-756-301B-3
19	484	86.9	107	2	US-09-756-398B-3
20	480	86.2	143	1	US-08-653-402B-8
21	477	85.6	106	1	US-08-326-362-4
22	438	78.6	107	1	US-08-436-463-20
23	438	78.6	108	2	US-09-233-290-27
24	438	78.6	109	1	US-07-942-245-4
25	435	78.1	107	1	US-08-107-669D-1
26	435	78.1	107	1	US-08-472-788A-1
27	435	78.1	107	1	US-08-477-531B-1

28	435	78.1	107	1	US-08-082-842A-1	Sequence 1, Appli
29	425	76.3	107	1	US-07-634-278-62	Sequence 62, Appl
30	425	76.3	107	1	US-08-477-728-62	Sequence 62, Appl
31	425	76.3	107	1	US-08-474-040-62	Sequence 62, Appl
32	425	76.3	107	1	US-08-487-200-62	Sequence 62, Appl
33	425	76.3	107	2	US-08-484-537-62	Sequence 62, Appl
34	425	76.3	127	1	US-07-634-278-83	Sequence 83, Appl
35	425	76.3	127	1	US-08-477-728-83	Sequence 83, Appl
36	425	76.3	127	1	US-08-474-040-83	Sequence 83, Appl
37	425	76.3	127	1	US-08-487-200-83	Sequence 83, Appl
38	425	76.3	127	2	US-08-484-537-83	Sequence 83, Appl
39	422	75.8	127	1	US-08-436-463-4	Sequence 4, Appli
40	417	74.9	127	1	US-08-476-176B-6	Sequence 6, Appli
41	417	74.9	127	2	US-08-127-721A-6	Sequence 6, Appli
42	417	74.9	127	2	US-08-485-246A-6	Sequence 6, Appli
43	415	74.5	127	1	US-08-436-463-18	Sequence 18, Appl
44	413	74.1	127	1	US-08-476-176B-8	Sequence 8, Appli
45	413	74.1	127	2	US-08-127-721A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-476-176B-4
Sequence 4, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/R/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-4
Query Match 89.4%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DILLTOSPALISVSPGERVSPSCRTSOSIGTNIMHYOQRTNGFPRLLIKXVSESISGIPS 60
DB 1 DILLTOSPALISVSPGERVSPSCRTSOSIGTNIMHYOQRTNGFPRLLIKXVSESISGIPS 60
QY 61 RFSGSGGTDFILINSVSESDIADYYCOQSNTPFTFGGKLEIK 107
DB 61 RFSGSGGTDFILINSVSESDIADYYCOQSDSWPTTGGGKLEIK 107

RESULT 2
US-08-127-721A-4
Sequence 4, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-127-721A-4

Query Match 89.4%; Score 498; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-4

Query Match 89.4%; Score 498; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DILLTOSPALISVSPGERVSPSCRTSOSIGTNIMHYOQRTNGFPRLLIKXVSESISGIPS 60
DB 1 DILLTOSPALISVSPGERVSPSCRTSOSIGTNIMHYOQRTNGFPRLLIKXVSESISGIPS 60
QY 61 RFSGSGGTDFILINSVSESDIADYYCOQSNTPFTFGGKLEIK 107
DB 61 RFSGSGGTDFILINSVSESDIADYYCOQSDSWPTTGGGKLEIK 107

RESULT 4
US-09-244-369B-1
Sequence 1, Application US/09244369B
Patent No. 6418338
GENERAL INFORMATION:
APPLICANT: Barbera-Guillam, Emilio
TITLE OF INVENTION: Method for detecting and surgically removing lymphoid tissue invo
FILE REFERENCE: Phy-01
CURRENT APPLICATION NUMBER: US/09/244,369B
CURRENT FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: US 60/073,882
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: US 60/077,970
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:22:45 ; Search time 137.504 Seconds
(without alignments)
549.012 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILLTQSPALISVSPGERVS.....CQGSNTWPTFGGCTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	455	81.7	115 1	KVSI_MOUSE
2	395	70.9	262 2	Q65ZT1_MOUSE
3	358.5	64.4	235 2	Q6GMW0_HUMAN
4	357	64.1	108 2	Q9UL83_HUMAN
5	354.5	63.6	109 2	Q9UL85_HUMAN
6	353	63.4	108 2	Q8VIT0_MOUSE
7	350.5	62.9	109 1	KV3F_HUMAN
8	348.5	62.6	114 2	Q8K1F1_MOUSE
9	348	62.5	128 1	KV3K_HUMAN
10	347.5	62.4	129 1	KV3H_HUMAN
11	343	61.6	111 1	KV3H_MOUSE
12	339	60.9	111 2	Q5F2I7_MOUSE
13	338	60.7	111 2	Q920E9_MOUSE
14	338	60.7	238 2	Q6GJ57_MOUSE
15	335	60.1	111 1	KV3L_MOUSE
16	333	59.8	236 2	Q6GMX9_HUMAN
17	332.5	59.7	109 2	Q9UL78_HUMAN
18	332	59.6	108 1	KV1M_HUMAN
19	332	59.6	111 1	KV3M_MOUSE
20	332	59.6	111 1	KV3R_MOUSE
21	331.5	59.5	112 2	Q8K1F3_MOUSE
22	329.5	59.2	111 2	Q65ZN3_MOUSE
23	329	59.1	111 1	KV3O_MOUSE
24	328.5	59.0	235 2	Q6GMV9_HUMAN
25	327.5	58.8	237 2	Q56YV8_MOUSE
26	327	58.7	111 1	KV3S_MOUSE
27	326.5	58.6	129 1	KV3L_HUMAN
28	326	58.5	108 1	KV5K_MOUSE
29	326	58.5	108 1	KV5O_MOUSE
30	326	58.5	234 2	Q4KM66_RAT
31	326	58.5	236 2	Q6PIH7_HUMAN

32	325	58.3	236 2	Q6GMX8_HUMAN	Q6GMX8 homo sapien
33	324.5	58.3	134 2	Q8VDD0_MOUSE	Q8VDD0 mus musculus
34	324	58.2	108 1	KV5L_MOUSE	P01645 mus musculus
35	324	58.2	108 1	KV5N_MOUSE	P01647 mus musculus
36	324	58.2	108 2	Q9UL79_HUMAN	P01679 homo sapien
37	324	58.2	111 1	KV3N_MOUSE	P01666 mus musculus
38	324	58.2	111 1	KV3U_MOUSE	P01673 mus musculus
39	324	58.2	136 1	KV5E_MOUSE	P01634 mus musculus
40	323	58.0	108 1	KV1Y_HUMAN	P80362 homo sapien
41	323	58.0	111 1	KV3Q_MOUSE	P01669 mus musculus
42	323	58.0	111 2	Q811U6_MOUSE	Q811U6 mus musculus
43	323	58.0	234 2	Q7Z473_HUMAN	Q7Z473 homo sapien
44	322.5	57.9	107 2	Q96SA9_HUMAN	Q96SA9 homo sapien
45	322.5	57.9	108 1	KV3A_HUMAN	P01619 homo sapien

ALIGNMENTS

RESULT 1
KVSI_MOUSE STANDARD; PRT; 115 AA.

AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NCLEOTIDE SEQUENCE.
RX MEDLINE=81220975; PubMed=6264318;
RA Pech M., Hochtl J., Schneil H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism."
RL Nature 291:668-670(1981).
CC -I- MISCELLANEOUS: There appears to be two possible splice junctions at the 3' end of the intron. The alternate would code for a protein lacking residues 17-19.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

PIR; A01925; KVM5L7.
DR PDB; 1C08; X-ray; A=22-115.
DR PDB; 1IC4; X-ray; L=22-115.
DR PDB; 1IC5; X-ray; L=22-115.
DR PDB; 1IC7; X-ray; L=22-115.
DR PDB; 1J10; X-ray; L=22-115.
DR PDB; 1J1P; X-ray; L=22-115.
DR PDB; 1J1X; X-ray; L=22-114.
DR Ensembl; ENSMUSG00000029975; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT REGION 21 >115 Ig kappa chain V-V region L7.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Complementarity-determining-2.
FT REGION 70 76 Complementarity-determining-3.
FT REGION 77 108 Complementarity-determining-3.
FT REGION 109 >115 By similarity.
FT DISULFID 43 108
FT NON_TER 115 115

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2006, 17:32:01 ; Search time 22.9956 Seconds
(without alignments)
447.702 Million cell updates/sec

Title: US-10-524-134-4

Perfect score: 557

Sequence: 1 DILLTOSPAILSVSPGERVSVS.....COQSWTPFTGCGTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	90.3	108	2 C30502	Ig kappa chain V r
2	499	89.6	128	2 PNO445	Ig kappa chain pre
3	455	81.7	115	1 KVM5L7	Ig kappa chain pre
4	425	76.3	107	2 A45722	anti-glycoprotein
5	424	76.1	107	2 B45722	anti-glycoprotein
6	423	75.9	123	2 S35479	Ig kappa chain pre
7	421	75.6	106	2 PLO267	Ig kappa chain V r
8	418	75.0	102	2 S26346	Ig kappa chain V r
9	415	74.5	107	2 C45722	anti-glycoprotein
10	415	74.5	138	2 A26471	Ig kappa chain pre
11	408.5	73.3	87	2 PH1082	Ig light chain V r
12	408	73.2	104	2 B43413	Ig kappa chain V r
13	384	68.9	103	2 S19975	Ig kappa chain V r
14	377.5	67.8	215	2 J80244	Ig kappa chain V r
15	376	67.5	117	2 S40362	Ig kappa chain - h
16	370	66.4	144	2 PLO106	Ig kappa chain pre
17	365	65.5	128	2 S40343	Ig kappa chain V-J
18	360	64.6	111	2 S23828	Ig kappa chain V r
19	359	64.5	107	2 S34005	Ig kappa chain V r
20	357.5	64.2	2	2 S54905	Ig kappa chain V r
21	356	63.9	108	2 J80243	Ig kappa chain V r
22	354	63.6	108	2 S19674	Ig kappa chain V r
23	352	63.2	106	2 PCA282	Ig kappa chain (an
24	352	63.2	108	2 G44151	Ig kappa chain V r
25	352	63.2	128	2 A56701	Ig kappa chain V r
26	350.5	62.9	109	1 K3HUPM	Ig kappa chain V-I
27	349	62.7	125	2 S40344	Ig kappa chain V-J
28	348	62.5	128	1 K3H041	Ig kappa chain pre
29	348	62.5	129	2 S29627	Ig kappa chain V r

30	347	62.3	128	2 S40379	Ig kappa chain V-J
31	345	61.9	107	2 A28195	Ig kappa chain V r
32	343	61.6	111	1 KVM537	Ig kappa chain V r
33	342.5	61.5	109	2 G30607	Ig kappa chain V-I
34	342.5	61.5	131	2 S40328	Ig kappa chain - h
35	342	61.4	128	2 S40345	Ig kappa chain V-J
36	341.5	61.3	116	2 B26555	Ig kappa chain V-I
37	341	61.2	108	2 PLO204	anti-DNA autoantib
38	341	61.2	125	2 S40349	Ig kappa chain V-J
39	340.5	61.1	120	2 S66536	Ig kappa chain V r
40	340	61.0	111	2 S05963	Ig kappa chain V-J
41	339	60.9	108	2 B49047	Ig kappa chain V r
42	339	60.9	117	2 S42466	Ig kappa chain V r
43	339	60.9	129	2 S40317	Ig kappa chain - h
44	339	60.9	132	2 S40334	Ig kappa chain - h
45	338	60.7	107	2 S36269	Ig lambda chain V

ALIGNMENTS

RESULT 1

C30502

Ig kappa chain V region (D444) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C/Accession: C30502

R:Ellat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A>Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A/Reference number: A30502; MUID:88315787; PMID:2457627

A/Accession: C30502

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <EIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 503; DB 2; Length 108;
Best Local Similarity 89.7%; Pred. No. 1.3e-38;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DILLTOSPAILSVSPGERVSVSFCRTSOSIGTINIMHYOORTNGFPLLIKVMSEISIGIPS 60

Db 1 DILLTOSPAILSVSPGERVSVSCRASQSIGTISIMHYOORTNGSPRLLIKVMSEISIGIPS 60

Qy 61 RFGSGSGTDFLTSTNSVSESDIADYCCOQSWTPFTGCGTKLEIK 107

Db 61 RFGSGSGTDFLTSTNSVSESDVADYCCOQINSWPRTGCGTKLEIK 107

RESULT 2

PNO445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C/Accession: PNO445

R:Kaluzs, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A>Title: A general method for chimerization of monoclonal antibodies by inverse polymerat

A/Reference number: PNO444; MUID:93138402; PMID:1339379

A/Accession: PNO445

A/Molecule type: mRNA

A/Residues: 1-128 <KAL>

A/Cross-references: UNIPARC:UPI0000176795; GB:I02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAY>

F:26-100/Domain: immunoglobulin homology <IMM>

```
Query Match      89.6%; Score 499; DB 2; Length 128;
Best Local Similarity 89.7%; Pred. No. 3.5e-38;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

Qy      1 DILLTSPALISVSPGERVVSFSCRTSOSIGTNIHWYQQRNGFPRLLIKNVSEISIGIPS 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 DVLITSPALISVSPGERVVSFSCRASOSIGTSIMHYQQRNGFPRLLIKTASESISIGIPS 70

```

```
QY      61 RESGSGSTDFILSNVSESDIADYYCQQSNTWPTFGGKLEIK 107
      |||||:|||||:|||||
Db      71 RESGSGSTDFILSNVSESDIADYYCQQTNSWPTFGGKLEIK 117
```

RESULT 3

IG kappa chain precursor V region (L7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1991 #sequence_revision 18-Dec-1991 #text_change 09-Jul-2004
C:Accession: A01925
R:Pech, M.; Hochtit, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1991
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences
A:Reference number: A93259; MUID:81220975; PMID:6264318
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PEC>
A:Cross-references: UNIPROT:P01642; UNIPARC:UP0000023365; GB:V01564; GB:J00574; NID:g551564
A:Note: the sequence was determined from the germ-line gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron, thus:
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 120 kDa superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
E:1-20/Domain: signal sequence #status: predicted <SIG>
F:21-115/Product: Ig kappa chain V region (L7) #status: predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMV>
F:43-108/Disulfide bonds: #status: predicted

Query Match	81.7%;	Score 455;	DB 1;	Length 115;
Best Local Similarity	92.6%;	Pred. No. 2.9e-34;		
Matches	88;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0

```

QY      1 DILLTSPAILSVSPGERVSPFSCCTQSQ:ICTNIMHWQQRINGFPRLLIKNVSEISIGIPS 60
      ||||| | | | | |
      |||||:|||||
      |||||
      |||||
Db      21 DILLTSPAILSVSPGERVSPFSCRASQSIGTSHWQQRINGSPRLLIKVASESISIGIPS 80

```

QY 61 RFGSGSGTDFILINSVESEDIADYYCCQSNTP 95
|||||:|
Db 81 RFGSGSGTDFILINSVESEDIADYYCCQSNTP 115

RESULT 4

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (first
A:55722
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez,
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on h
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Cross-references: UNIPARC:UPI0000144CFD
A:Note: sequence extracted from NCBI backbone (NCBI:120589)
C:Superfamily: Immunoglobulin V region, immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match	76.3%;	Score 425;	DB 2;	Length 107;
Best Local Similarity	-73.8%;	Pred. No. 1.4e-31;		
Matches	79;	Conservative	12;	Mismatches 16;
			Indels	0;
			Gaps	0;

Oy

1 DILTQSPALISVSPGERVSFSCRTSQSIGINIMHWQOORTNGPRLLIKXSESISGIPS 60
||:|||||:::||:||||:||||:||||:
Db

1 DIVLTQSPATISVTPEDSVSLSCRASQSISNNLHMWQQKSHESPRLLIKVASQSISGIPS 60

```
QY      61 RFSGSGSGTDFILSNVSESDIADYYCQQSNTWPFPPFGGGTKLEIK 107
      |||||:::||:||||:|||||
Db      61 RFSGSGSGTDFILSNVGVETEDFGMYFCQQSNSWPHFFGGGKLEIK 107
```

RESULT 5

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (Frederick)
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_rev150n 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpon, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human
A:Reference number: A45722; PMID:93100833; PMID:7677958
A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Cross-references: UNIPARC:UPI00001677AF
A>Note: Sequence extracted from NCBI backbone (NCBI:120590)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: glycoprotein
P:16-90/Domain: immunoglobulin homology <IMM>

Query Match	76.1%;	Score 424;	DB 2;	Length 107;
Best Local Similarity	73.8%;	Pred. No. 1.7e-31;		
Matches 79;	Conservative 13;	Mismatches 15;	Indels 0;	Gaps 0

```
QY      1 DILTQSPALISVSPGERVVSFSCRTSQSIGTNIHWQQRKTNGPRLLIKVSSESISGIPS 60
      ||:|||||:||||: || ||||| ||| :|||||: ||||| ||| :|||||
Db      1 DIVLTQSPALISVTPGDSVSLSCRASQISINNIHWQQRKSHSPRLLIKVASQISIGIPS 60
```

QY 61 RFSSGSGTDFILSINSVESEDIADYYCQQSNTWPFREGGTLEIK 107
| | | | | : | | | | : | | | | |
Db 61 RFSGGSGTDFLTINSVETEDFGMYFCOOTNSMPPHFGGSITLEIK 107

RESULT

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #ext_change 21-Jan-2000
C:Accession: S35479
R:Takeeda, Y.; Wise, K.S.; Hoffman, R.W.
N:Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mouse
A:Reference number: S35479; MUID:92375706; PMID:1387203
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <7TK>
A:Cross-references: UNIPARC:UPI0000115359; EMBL:M93959; NID:G197572; PIDN:AAA39079.1; PIR:G197572
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domains: signal sequence (fragment) #status predicted <SIG>
F:113-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match	75.9%	Score 423;	DB 2;	Length 123;
Best Local Similarity	74.8%	Pred. No. 2.4e-31;		
Matches	80;	Conservative	15;	Indels 0; Gaps 0

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:22:00 ; Search time 262.338 Seconds
(without alignments)
179.210 Million cell updates/sec

Title: US-10-524-134-4

Perfect score: 557
Sequence: 1 DILLTGSPALSVSPGRVS.....CQGSNTWPTFGGSKLEIK 107

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	100.0	107	ADL00215	Adl00215 Human Fcg
2	510	91.6	214	AEC20776	Aec20776 M-CSF spe
3	504	90.5	107	ADY31675	Ady31675 Anti-IL9
4	504	90.5	108	ADG75665	Adg75665 Humanised
5	504	90.5	109	AEC20766	Aec20766 M-CSF spe
6	504	90.5	214	AEC20765	Aec20765 M-CSF spe
7	503	90.3	107	AAB10023	Aab10023 H. pylori
8	503	90.3	107	AAB86109	Aab86109 H. pylori
9	503	90.3	107	AAB86071	Aab86071 H. pylori
10	503	90.3	107	ABB99221	Abb99221 Part of c
11	503	90.3	107	ADY80249	Ady80249 Fragment
12	503	90.3	107	AEC07204	Aec07204 Murine NY
13	503	90.3	124	AEC07178	Aec07178 NYR-1002
14	503	90.3	214	ABB99223	Abb99223 ChimERIC
15	503	90.3	214	ADY80251	Ady80251 Amino aci
16	500	89.8	107	AAU72850	Aau72850 Human p53
17	500	89.8	510	AAU72860	Aau72860 Human p53
18	499	89.6	107	AAR31219	Aar31219 Anti-IL2R
19	499	89.6	107	ADJ80369	Adj80369 Antibody
20	499	89.6	107	AEA48149	Aea48149 Mouse ant
21	499	89.6	107	AEI13698	Aei13698 Human ant
22	499	89.6	127	AAW08945	Aaw08945 Kappa lig
23	499	89.6	127	AAW08941	Aaw08941 Kappa lig
24	499	89.6	127	AAW08943	Aaw08943 Kappa lig

25	499	89.6	234	8	ADS14301	Adsl4301 EGFR lig
26	499	89.6	236	8	ADP44635	Adp44635 Murine an
27	499	89.6	236	9	AEA60461	Aea60461 Mouse ant
28	498	89.4	107	2	AAR50190	Aar50190 Light cha
29	498	89.4	107	2	AAZ26979	Aaz26979 Light cha
30	498	89.4	107	8	ADR43401	Adr43401 Murine an
31	498	89.4	107	8	ADR31546	Adr31546 Murine TR
32	498	89.4	107	8	ADR87520	Adr87520 Mouse ant
33	498	89.4	107	9	AEC08122	Aec08122 Murine m
34	498	89.4	242	4	AAB31426	Aab31426 Protein u
35	498	89.4	244	4	AAZ31610	Aaz31610 Mucin Tn
36	498	89.4	244	4	AAZ31425	Aaz31425 Protein u
37	497	89.2	107	5	AAU72842	Aau72842 Anti-NGK2
38	497	89.2	510	5	AAU72859	Aau72859 6ESR74-7
39	496	89.0	107	7	ADJ80370	Adj80370 FR homolo
40	495	88.9	651	2	AAW05135	Aaw05135 scFv(225)
41	495	88.9	892	2	AAW05140	Aaw05140 scFv2(225)
42	495	88.9	892	2	AAW05139	Aaw05139 scFv2 (PRP
43	495	88.9	1020	2	AAW05141	Aaw05141 scFv2 (PRP
44	494	88.7	127	2	AAW44176	Aaw44176 Monoclonal
45	493	88.5	106	9	AEA40019	Aea40019 Mouse ant

ALIGNMENTS

RESULT 1
ADL00215 standard; protein; 107 AA.
ID ADL00215
XX
AC ADL00215;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human FcgammaRIIB antibody light chain.
XX
KW cytosolic; antirheumatic; antiarthritic; antipsoriatic; dermatological;
KW immunosuppressive; antinflammatory; antiaesthetic; antiallergic;
KW immunosuppressive; nephrotropic; ophtalmological;
KW B cell receptor-mediated signaling modulator;
KW Fc gamma RI-induced mast cell activation modulator;
KW B cell activation modulator; B cell proliferation modulator;
KW antibody production modulator; intracellular calcium influx modulator;
KW vaccine composition efficacy enhancer; gene therapy; FcgammaRIIB; cancer;
KW breast cancer; ovarian cancer; prostate cancer; cervical cancer;
KW pancreatic cancer; chemotherapy; immunotherapy; radiation therapy;
KW hormonal therapy; autoimmune disorder; rheumatoid arthritis;
KW psoriatic arthritis; ankylosing spondylitis; Rieker's Syndrome;
KW psoriasis; lupus erythematosus; IGF-mediated allergic disorder; asthma;
KW allergic rhinitis; gastrointestinal allergy; eosinophilia;
KW conjunctivitis; glomerular nephritis; autoimmune disease; vaccine;
KW B cell malignancy; non-Hodgkin's lymphoma; solid tumour;
KW fragment of crystallisation gamma receptor IIB; antibody light chain;
human.
XX
OS Homo sapiens.
XX
PN WO2004016750-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025339.
XX
PR 14-AUG-2002; 2002US-0403266P.
XX
PA (MACR-) MACROGENICS INC.
XX
PI Koenig S, Veri M;
XX WPI; 2004-203783/19.
XX N-PSDB; ADL00214.
XX Novel isolated antibody or its fragment useful for treating diseases

PT e.g., cancer, that specifically binds native Fc γ mmarIIIB with greater
 PT affinity than antibody or its fragment that binds native Fc γ mmarIIIA.
 XX
 PS Disclosure; SEQ ID NO 4; 174pp; English.

CC The invention describes an isolated antibody or its fragment (I) that
 CC specifically binds native Fc γ mmarIIIB. (I) is useful for treating cancer
 CC (e.g., breast, ovarian, prostate, cervical or pancreatic cancer) in a
 CC patient (e.g., human) having cancer with specific cancer antigen which
 CC involves administering a first antibody or its fragment which is (I) and
 CC a second antibody that specifically binds the cancer antigen and is
 CC cytotoxic. The above method further involves administration of one or
 CC more additional cancer therapies such as chemotherapy, immunotherapy,
 CC radiation therapy, hormonal therapy, or surgery. (I) is useful for
 CC treating an autoimmune disorder e.g., rheumatoid arthritis, psoriatic
 CC arthritis, ankylosing spondylitis, Reiter's Syndrome, psoriasis, or lupus
 CC erythematosus. The above method further involves administering to the
 CC patient a therapeutically effective amount of one or more anti-
 CC inflammatory agents or immunomodulatory agents e.g., small organic
 CC molecule such as methotrexate or corticosteroid. The anti-inflammatory
 CC agent is a non-steroidal anti-inflammatory drug e.g. aspirin or
 CC ketoprofen. (I) is also useful for: treating IGE-mediated allergic
 CC disorder such as asthma, allergic rhinitis, gastrointestinal allergies,
 CC eosinophilia, conjunctivitis, or glomerular nephritis; enhancing an
 CC antibody mediated cytotoxic effect in a subject; diagnosing an autoimmune
 CC disease in a subject; enhancing an immune response to a vaccine
 CC composition in a subject; treating a B cell malignancy (e.g., non-
 CC Hodgkin's lymphoma); treating a disease in a patient; treating a solid
 CC tumour in a patient; and treating cancer in a patient. (I) has an altered
 CC affinity for an Fc γ mmar. (I) antibody binds Fc γ mmarIIIA with a higher
 CC affinity than a comparable antibody comprising a wild-type Fc region
 CC binds Fc γ mmarIIIA. (I) has an enhanced antibody mediated effector
 CC function relative to a comparable antibody comprising a wild-type Fc
 CC region. This is the amino acid sequence of human fragment of
 CC crystallization gamma receptor IIB (Fc γ mmarIIB) antibody light chain.
 CC
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 557; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 6.7e-41;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILLTQSPALISVSGERVSFCRTSOSIGTNIHMYQORTNGFPLLLIKNVSISIGIPS 60
 DB 1 DILLTQSPALISVSGERVSFCRTSOSIGTNIHMYQORTNGFPLLLIKNVSISIGIPS 60
 QY 61 RFSGSGSTDFLLINSVSESDIADYYCQGSNTWPFRTGGGTKLEIK 107
 DB 61 RFSGSGSTDFLLINSVSESDIADYYCQGSNTWPFRTGGGTKLEIK 107

RESULT 2
 AEC20776 ID AEC20776 standard; protein; 214 AA.

AC AEC20776;

XX 20-OCT-2005 (first entry)

DE M-CSF specific murine antibody MC-3 light chain SEQ ID NO 15.

XX endocrine-gen.; antihypertic; antibacterial; antiinflammatory;
 KW antirheumatic; antitumor; bone metastases; calcium antagonist; cancer;
 KW cardiovascular-gen.; degeneration; eating-disorders-gen.;
 KW endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.;
 KW genetic disorder; light chain; hepatotropic; hypercalcemia;
 KW immune disease; immunotherapy; inflammation; monoclonal antibody;
 KW mouth disease; musculoskeletal disease; neoplasm; nephrotropic;
 KW osteopathic; osteoporosis; osteoporosis; pager disease;
 KW periodontal disease; pharmaceutical; rheumatoid arthritis; MC-3.

XX Mus musculus.

OS

PN WO2005068503-A2.

XX 28-JUL-2005.

XX 06-JAN-2005; 2005WO-US000546.

XX 07-JAN-2004; 2004US-0535181P.

PR 02-JUN-2004; 2004US-0576417P.

XX (CHIR) CHIRON CORP.

PA (XOMA) XOMA TECHNOLOGY LTD.

XX Liu C, Zimmerman DL, Harrowe GM, Kotche K, Kavanaugh WM, Long L;

PI Calderon-Cacia M, Horwitz AH;

PT WPI; 2005-597707/61.

XX Example 10; SEQ ID NO 15; 269pp; English.

XX The invention describes a non-murine antibody (I) that competes with

CC monoclonal antibody RX1 for binding to macrophage colony stimulating

CC factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has

CC the heavy chain and light chain amino acid sequences having a fully

CC defined 447 amino acids (SEQ ID NO. 2) and 214 amino acids (SEQ ID NO. 4)

CC sequences given in the specification, respectively. (I) is useful for

CC preventing a subject afflicted with a disease that causes or contributes

CC to osteolysis, where the antibody effectively reduces the severity of

CC bone loss associated with the disease. The disease is chosen from

CC metabolic bone diseases associated with relatively increased osteoclast

CC activity, including endocrinopathies, hypercalcemia, deficiency states,

CC chronic diseases, and hereditary diseases, cancer, osteoporosis,

CC osteopetrosis, inflammation of bone associated with arthritis and/or

CC rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or

CC Paget's disease. (I) is useful for preventing or treating metastatic

CC cancer. Antibodies of the invention are useful for preventing or reducing

CC bone loss; osteolysis; metastatic cancer to bone and cancer (I) is

CC useful for manufacturing a medicament for preventing or reducing bone

CC loss in a patient exhibiting osteolysis, manufacturing a medicament for

CC treating a patient afflicted with a disease that causes or contributes to

CC osteolysis, and metastatic cancer to bone in a patient suffering from

CC metastatic cancer, for manufacturing a medicament for treating a patient

CC having cancer. (I) in synergistic combination, is useful for preparing a

CC medicament for treating a patient exhibiting osteolysis. This is the

CC amino acid sequence of macrophage colony stimulating factor (M-CSF)

XX specific murine antibody MC-3 light chain.

SQ Sequence 214 AA;

Query Match 91.6%; Score 510; DB 9; Length 214;

Best Local Similarity 92.5%; Pred. No. 1.7e-36;

Matches 99; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DILLTQSPALISVSGERVSFCRTSOSIGTNIHMYQORTNGFPLLLIKNVSISIGIPS 60
 DB 1 DILLTQSPALISVSGERVSFCRTSOSIGTNIHMYQORTNGFPLLLIKNVSISIGIPS 60
 QY 61 RFSGSGSTDFLLINSVSESDIADYYCQGSNTWPFRTGGGTKLEIK 107
 DB 61 RFSGSGSTDFLLINSVSESDIADYYCQGSNTWPFRTGGGTKLEIK 107

RESULT 3

ADY31675 ID ADY31675 standard; protein; 107 AA.

AC ADY31675;

XX 05-MAY-2005 (first entry)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:53:06 ; Search time 11.6754 Seconds
(without alignments)
147.285 Million cell updates/sec

Title: US-10-524-134-2

Perfect score: 651
Sequence: 1 QVQLQCPVTELVIRPGASVMTL.....SDYYSGMDYWGQSTVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	121	7	US-11-108-135-28 Sequence 28, Appl
2	651	100.0	121	7	US-11-126-978-28 Sequence 28, Appl
3	529	81.3	121	7	US-11-108-135-24 Sequence 24, Appl
4	529	81.3	121	7	US-11-126-978-24 Sequence 24, Appl
5	502.5	77.2	122	6	US-10-932-334-73 Sequence 73, Appl
6	460.5	70.7	118	7	US-11-126-798-48 Sequence 48, Appl
7	457.5	70.3	120	6	US-10-932-334-72 Sequence 72, Appl
8	453	69.6	113	7	US-11-177-648-7 Sequence 7, Appl
9	453	69.6	462	7	US-11-177-648-9 Sequence 9, Appl
10	452.5	69.5	120	6	US-10-932-334-71 Sequence 71, Appl
11	452.5	68.9	248	6	US-10-512-184-36 Sequence 36, Appl
12	452.5	69.5	615	6	US-10-512-184-50 Sequence 50, Appl
13	450.5	69.2	120	6	US-10-983-357-3 Sequence 3, Appl
14	450	69.1	119	7	US-11-221-900-10 Sequence 10, Appl
15	449	69.0	117	6	US-10-932-334-76 Sequence 76, Appl
16	448.5	68.9	120	6	US-10-932-334-74 Sequence 74, Appl
17	448.5	68.9	120	6	US-10-932-334-78 Sequence 78, Appl
18	445.5	68.4	124	6	US-10-932-334-7 Sequence 7, Appl
19	445.5	68.4	124	6	US-10-932-334-13 Sequence 13, Appl
20	445.5	68.4	124	6	US-10-932-334-70 Sequence 70, Appl
21	445.5	68.4	143	6	US-10-932-334-52 Sequence 52, Appl
22	444	68.2	666	6	US-10-981-356A-29 Sequence 29, Appl
23	444	68.2	667	7	US-11-096-046-29 Sequence 29, Appl
24	441.5	67.8	116	7	US-11-055-163-17 Sequence 17, Appl
25	441.5	67.8	123	6	US-10-932-334-87 Sequence 87, Appl

26	441.5	67.8	123	6	US-10-932-334-88 Sequence 88, Appl
27	441.5	67.8	123	6	US-10-932-334-92 Sequence 92, Appl
28	441	67.7	121	6	US-10-507-662-26 Sequence 26, Appl
29	436	67.0	121	6	US-10-507-662-25 Sequence 25, Appl
30	435	66.8	116	7	US-11-097-812-19 Sequence 19, Appl
31	435	66.8	121	7	US-11-107-028-35 Sequence 35, Appl
32	432.5	66.4	129	7	US-11-179-820-4 Sequence 4, Appl
33	432	66.4	121	6	US-10-932-334-81 Sequence 81, Appl
34	430.5	66.1	120	6	US-10-507-662-61 Sequence 61, Appl
35	429.5	66.0	118	6	US-10-932-334-75 Sequence 75, Appl
36	429	65.9	121	6	US-10-665-658-4 Sequence 4, Appl
37	429	65.9	121	7	US-11-107-028-52 Sequence 52, Appl
38	429	65.9	121	7	US-11-149-031-4 Sequence 4, Appl
39	429	65.9	133	7	US-11-069-834-2 Sequence 2, Appl
40	428	65.7	247	7	US-11-084-717-21 Sequence 21, Appl
41	428	65.7	247	7	US-11-179-244-21 Sequence 21, Appl
42	428	65.7	247	7	US-11-084-055B-21 Sequence 21, Appl
43	427.5	65.7	111	7	US-11-097-812-205 Sequence 205, Appl
44	427.5	65.7	120	6	US-10-932-334-77 Sequence 77, Appl
45	423	65.0	113	7	US-11-177-648-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-11-108-135-28
Sequence 28, Application US/11108135
Publication No. US20050260213A1
GENERAL INFORMATION:
APPLICANT: Koenig, Scott
APPLICANT: Veri, Maria Concetta
APPLICANT: Tualillon, Nadine
APPLICANT: Bonvini, Ezio
APPLICANT: Stavenhagen, Jeffrey
APPLICANT: Rankin, Christopher
TITLE OR INVENTION: R γ -gamma-R11B-specific antibodies and methods of use thereof
FILE REFERENCE: 11183-014-999
CURRENT APPLICATION NUMBER: US/11/108,135
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/562,804
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/582,044
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/582,045
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/654,713
PRIOR FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatsSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 121
TYPE: PRT
ORGANISM: mus sp.
FEATURE:
OTHER INFORMATION: Mouse 286 heavy chain variable region
US-11-108-135-28

Query Match 100.0%; Score 651; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,2e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 1 QVQLQCPVTELVIRPGASVMTLSCRASDYPFTNWIHWKORPGGLEWIGVIDPSDTPNY 60
Db 1 QVQLQCPVTELVIRPGASVMTLSCRASDYPFTNWIHWKORPGGLEWIGVIDPSDTPNY 60
Query 61 NKKFKGATLTIVVSSSTAYMOLSLTSDSAVYYCARNDSDPYSGMDYWGQSTVTVS 120
Db 61 NKKFKGATLTIVVSSSTAYMOLSLTSDSAVYYCARNDSDPYSGMDYWGQSTVTVS 120
Query 121 S 121
Db 121 S 121

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RESULT 2
US-11-126-978-28
; Sequence 28, Application US/11126978
; Publication No. US20060013810A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie Sydnor
; APPLICANT: Huang, Ling
; TITLE OF INVENTION: HUMANIZED Fc-gammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THEREOF
; FILE REFERENCE: 11183-018-999
; CURRENT APPLICATION NUMBER: US/11/126,978
; PRIOR FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 60/582,043
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/569,882
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse 2B6 heavy chain variable region
US-11-126-978-28

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Best Local Similarity 100.0%; Pred. No. 2,2e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  QVQLQQPTVELVRPGASVWLSCKASDYPFTNYWIMHWKRPQGGLGEMIGVIDPSDTYPNY 60
Db      1  QVQLQQPTVELVRPGASVWLSCKASDYPFTNYWIMHWKRPQGGLGEMIGVIDPSDTYPNY 60

QY      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120
Db      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120

QY      121  S 121
Db      121  S 121

RESULT 3
US-11-108-135-24
; Sequence 24, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuallion, Madine
; APPLICANT: Bonvin, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/554,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
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; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-108-135-24

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Best Local Similarity 78.5%; Pred. No. 2,3e-37;
Matches 95; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY      1  QVQLQQPTVELVRPGASVWLSCKASDYPFTNYWIMHWKRPQGGLGEMIGVIDPSDTYPNY 60
Db      1  QVQLVQSGAEVKKPKGASVWLSCKASGYTFITNYIMHWKRAQPGGLGEMIGVIDPSDTYPNY 60

QY      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120
Db      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120

QY      121  S 121
Db      121  S 121

RESULT 4
US-11-126-978-24
; Sequence 24, Application US/11126978
; Publication No. US20060013810A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie Sydnor
; APPLICANT: Huang, Ling
; TITLE OF INVENTION: HUMANIZED Fc-gammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THEREOF
; FILE REFERENCE: 11183-018-999
; CURRENT APPLICATION NUMBER: US/11/126,978
; PRIOR FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 60/582,043
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/569,882
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-126-978-24

Query Match      81.3%; Score 529; DB 7; Length 121;
Best Local Similarity 78.5%; Pred. No. 2,3e-37;
Matches 95; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY      1  QVQLQQPTVELVRPGASVWLSCKASDYPFTNYWIMHWKRPQGGLGEMIGVIDPSDTYPNY 60
Db      1  QVQLVQSGAEVKKPKGASVWLSCKASGYTFITNYIMHWKRAQPGGLGEMIGVIDPSDTYPNY 60

QY      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120
Db      61  NKKFGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVTS 120

QY      121  S 121
Db      121  S 121

RESULT 5
US-10-932-334-73
; Sequence 73, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:52:22 ; Search time 119.939 Seconds
(without alignments)
421.527 Million cell updates/sec

Title: US-10-524-134-2

Perfect score: 651

Sequence: 1 QVQLQQPVTELVPRGASVWL.....SDYSGMDYWGQSTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	121	4	US-10-643-857-2 Sequence 2, Appli
2	651	100.0	121	5	US-10-524-134-2 Sequence 2, Appli
3	502.5	77.2	122	5	US-10-729-441-73 Sequence 73, Appli
4	502.5	77.2	122	5	US-10-897-406-73 Sequence 73, Appli
5	492.5	75.7	242	4	US-10-259-087A-18 Sequence 18, Appli
6	492.5	75.7	242	4	US-10-689-006-18 Sequence 18, Appli
7	491.5	75.5	118	5	US-10-816-938-23 Sequence 23, Appli
8	489	75.1	140	3	US-09-748-960-4 Sequence 4, Appli
9	487	74.8	464	4	US-10-216-484-9 Sequence 9, Appli
10	487	74.8	464	4	US-10-384-933-9 Sequence 9, Appli
11	483.5	74.3	120	4	US-10-096-246-12 Sequence 12, Appli
12	472	72.0	143	5	US-10-010-729-66 Sequence 66, Appli
13	469	72.0	365	5	US-10-880-028-44 Sequence 44, Appli
14	469	72.0	365	5	US-10-880-320-44 Sequence 44, Appli
15	467.5	71.8	118	4	US-10-435-614-11 Sequence 11, Appli
16	467.5	71.8	260	4	US-10-435-614-20 Sequence 20, Appli
17	466.5	71.7	467	4	US-10-742-405-12 Sequence 12, Appli
18	464.5	71.4	122	2	US-08-779-784-28 Sequence 28, Appli
19	462.5	71.0	143	5	US-10-895-135-63 Sequence 63, Appli
20	461	70.8	118	2	US-08-779-784-26 Sequence 26, Appli
21	458.5	70.4	118	4	US-10-436-782-5 Sequence 5, Appli
22	458.5	70.4	118	6	US-11-004-795A-5 Sequence 5, Appli
23	458.5	70.4	118	6	US-11-004-794A-5 Sequence 5, Appli
24	458.5	70.4	121	5	US-10-879-994-8 Sequence 82, Appli
25	458.5	70.4	248	5	US-10-879-994-14 Sequence 14, Appli
26	458.5	70.4	248	5	US-10-610-452-14 Sequence 14, Appli
27	457.5	70.3	118	4	US-10-435-614-13 Sequence 13, Appli

28	457.5	70.3	120	4	US-10-351-748-24 Sequence 24, Appli
29	457.5	70.3	120	5	US-10-351-748-24 Sequence 24, Appli
30	457.5	70.3	120	5	US-10-729-441-72 Sequence 72, Appli
31	457.5	70.3	120	5	US-10-897-406-72 Sequence 72, Appli
32	457.5	70.3	122	4	US-10-096-246-10 Sequence 10, Appli
33	457.5	70.3	122	4	US-10-096-246-11 Sequence 11, Appli
34	457.5	70.3	177	4	US-10-435-614-21 Sequence 21, Appli
35	455	69.9	138	3	US-09-753-436-78 Sequence 78, Appli
36	455	69.9	138	4	US-10-163-942-78 Sequence 78, Appli
37	455	69.9	138	5	US-10-745-115-78 Sequence 78, Appli
38	452.5	69.5	118	5	US-10-789-090-9 Sequence 9, Appli
39	452.5	69.5	120	5	US-10-729-441-71 Sequence 71, Appli
40	452.5	69.5	120	5	US-10-895-135-57 Sequence 57, Appli
41	452.5	69.5	120	5	US-10-897-406-71 Sequence 71, Appli
42	451.5	69.4	126	4	US-10-312-316-44 Sequence 44, Appli
43	450.5	69.2	120	5	US-10-842-011-3 Sequence 3, Appli
44	450	69.1	116	3	US-09-940-727B-17 Sequence 17, Appli
45	450	69.1	119	3	US-09-795-515-30 Sequence 30, Appli

ALIGNMENTS

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US-10-643-857-2
; Sequence 2, Application US/10643857
; Publication No. US20040185045A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; TITLE OR INVENTION: Anti-FcγRIIB monoclonal antibodies and their use in enhancing
; TITLE OR INVENTION: Immune response
; FILE REFERENCE: 11183-010-999
; CURRENT APPLICATION NUMBER: US/10/643,857
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,266
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-643-857-2

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Best Local Similarity 100.0%; Pred. No. 9e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 QVQLQQPVTELVPRGASVWLSCRASDYPFTNYIHWKORPGGLEWIGVIDPSDTPNY 60

QY      61 NKKFKGATLTIVVSSSTAYMQLSLTSDSAVYYCARNDSDYSGMDYWGQSTVTSS 120
        |||
Db       61 NKKFKGATLTIVVSSSTAYMQLSLTSDSAVYYCARNDSDYSGMDYWGQSTVTSS 120

QY      121 S 121
        |
Db       121 S 121

RESULT 2
US-10-524-134-2
; Sequence 2, Application US/10524134
; Publication No. US20050215767A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; TITLE OR INVENTION: Anti-FcγRIIB monoclonal antibodies and their use in enhancing
; TITLE OR INVENTION: Immune response
; FILE REFERENCE: 11183-003-999
; CURRENT APPLICATION NUMBER: US/10/524,134
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; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: PCT/US03/25339
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,266
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; OS-10-524-134-2

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Query Match	100.0%	Score 651;	DB 5;	Length 121;
Best Local Similarity	100.0%	Pred. NC. 9e-52;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 QVQLQQPTTELVRPGASVWLSCKASDYPETNNVHIVVKORPGGLEWISGVIDPSDITYPNV 60

Db 1 QVQLQQPTTELVRPGASVWLSCKADYDPTNNVHIVVKORPGGLEWISGVIDPSDITYPNV 60

QY 61 NKKEFGKATLTVVSSSTAYMQLSLTSDDSAVVYCARNGSDSYSGMDYGGGTSVTVS 120

Db 61 NKKEFGKATLTVVSSSTAYMQLSLTSDDSAVYCARNGSDSYSGMDYGGGTSVTVS 120

QY 121 S 121

Db 121 S 121

RESULT 3
US-10-729-441-73
; Sequence 73, Application US/10729441
; Publication No. US20040265307A1

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1  TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
2  FILE REFERENCE: A6899
3  CURRENT APPLICATION NUMBER: US/10/729,441
4  CURRENT FILING DATE: 2003-12-08
5  PRIOR APPLICATION NUMBER: 10/170,390
6  PRIOR FILING DATE: 2002-06-14
7  NUMBER OF SEQ ID NOS: 96
8  SOFTWARE: PatentIn version 3.2
9  SEQ ID NO 73
10 LENGTH: 122
11 TYPE: PRT
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: synthetic antibody structure
15 US-10-729-441-73

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Query Match	77.2%	Score 502.5	DB 5	Length 122
Best Local Similarity	78.6%	Pred: No. 3.3e-38		
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				Gaps 2

[illegible]

RESULT 4
US-10-897-406-73
; Sequence 73, Application US/10897406
; Publication No. US20050186203A1

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: GENERAL INFORMATION:
: APPLICANT: Immunogen, Inc.
: TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
: FILE REFERENCE: A8338
: CURRENT APPLICATION NUMBER: US/10/897,406
: PRIORITY FILING DATE: 2004-07-23
: PRIOR APPLICATION NUMBER: US/10/170,390
: PRIOR FILING DATE: 2002-06-14
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 73
: LENGTH: 122
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: synthetic antibody structure
: US-10-897-406-73

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Query Match	77.2%	Score 502.5	DB 5	Length 122
Best Local Similarity	78.6%	Pred. No. 3	3e-38	
Matches 99	Conservative	7	Mismatches 11	Indels 9
				Gaps 2

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Db	1	QVOLOQPPAEILYKPGASVYKLSCKASGYFTFSYMHMHVKGPEQGLEWIGVIDPSDTPY	60
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Qy	61	NKKRKGKATLVVSSSTAYMQLSLTSDSAVYVCARNGSDYYSG-----MDYWGQST	115
		:	
Db	61	NEKRKGKATLVVSSSTAYMQLSLTSDSAVYCA-----SLYYGTSYGVLDYWGQST	116
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Qy		SVTVSS 121	
Db		SVTVSS 122	

RESULT 5
US-10-259-087A-18
; Sequence 18, Application US/10259087A
; Publication No. US20030130190A1

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? APPLICANT: Vanderbilt University
? APPLICANT: Hallahan, Dennis E
? APPLICANT: Ou, Shmihian
? TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
? FILE REFERENCE: 1242/47/2
? CURRENT APPLICATION NUMBER: US/10/259,087A
? CURRENT FILING DATE: 2002-09-27
? PRIOR APPLICATION NUMBER: US 60/328123
? PRIOR FILING DATE: 2001-10-03
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 18
? LENGTH: 242
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Artificial antibody ligand number 1
? US-10-259-087A-18

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Query Match	75.7%	Score 492.5;	DB 4,	Length 242;
Best Local Similarity	77.7%	Pred. No. 5.7e-37;		
Matches 94; Conservative	9;	Mismatches 15;	Indels 3;	Gaps 1

[illegible]

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2006, 17:36:50 ; Search time 35.0263 Seconds
(without alignments)
285.607 Million cell updates/sec

Title: US-10-524-134-2

Perfect score: 651
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	493	75.7	119	1	US-08-553-497A-12	Sequence 12, Appl
2	483.5	74.3	120	2	US-10-092-246-12	Sequence 12, Appl
3	483.5	74.3	120	2	US-10-096-246A-12	Sequence 12, Appl
4	481	73.9	119	1	US-08-553-497A-8	Sequence 8, Appl
5	477	73.3	119	2	US-08-881-037-62	Sequence 62, Appl
6	477	73.3	445	1	US-08-353-400-33	Sequence 33, Appl
7	477	73.3	464	1	US-08-353-400-36	Sequence 36, Appl
8	475	73.0	119	2	US-08-881-037-60	Sequence 60, Appl
9	474	72.8	119	2	US-08-881-037-61	Sequence 61, Appl
10	474	72.8	288	2	US-09-423-439-38	Sequence 38, Appl
11	474	72.8	673	2	US-09-423-439-32	Sequence 32, Appl
12	473	72.7	119	2	US-08-881-037-63	Sequence 63, Appl
13	471	72.4	119	2	US-09-406-532-2	Sequence 2, Appl
14	466	71.6	119	2	US-09-254-180C-16	Sequence 16, Appl
15	466	71.6	119	2	US-09-254-180C-149	Sequence 149, App
16	466	71.6	119	2	US-08-913-555-23	Sequence 23, Appl
17	466	71.6	138	2	US-09-254-180C-143	Sequence 143, App
18	466	71.6	219	2	US-09-254-180C-180	Sequence 180, App
19	464.5	71.4	122	1	US-08-236-520-9	Sequence 9, Appl
20	464.5	71.4	122	4	PCT-US95-05262-9	Sequence 9, Appl
21	463	71.1	111	2	US-08-881-037-14	Sequence 14, Appl
22	463	71.1	118	2	US-09-065-059-5	Sequence 5, Appl
23	463	71.1	118	2	US-08-913-555-5	Sequence 5, Appl
24	461	70.8	111	2	US-08-881-037-15	Sequence 15, Appl
25	461	70.8	143	1	US-08-236-520-7	Sequence 7, Appl
26	461	70.8	143	4	PCT-US95-05262-7	Sequence 7, Appl
27	460.5	70.7	118	2	US-08-766-350B-48	Sequence 48, Appl

28	460.5	70.7	269	1	US-08-428-257A-72	Sequence 72, Appl
29	460.5	70.7	269	1	US-08-491-988-3	Sequence 3, Appl
30	460.5	70.7	402	1	US-08-491-988-9	Sequence 9, Appl
31	460.5	70.7	415	1	US-08-491-988-7	Sequence 7, Appl
32	460.5	70.7	435	1	US-08-491-988-5	Sequence 5, Appl
33	460	70.7	111	2	US-08-881-037-16	Sequence 16, Appl
34	459	70.5	111	2	US-08-881-037-17	Sequence 17, Appl
35	457.5	70.3	122	2	US-10-092-246-10	Sequence 10, Appl
36	457.5	70.3	122	2	US-10-092-246-11	Sequence 11, Appl
37	457.5	70.3	122	2	US-10-096-246A-10	Sequence 10, Appl
38	457.5	70.3	122	2	US-10-096-246A-11	Sequence 11, Appl
39	456.5	70.1	241	1	US-08-235-838-11	Sequence 11, Appl
40	456.5	70.1	241	1	US-08-465-473B-11	Sequence 11, Appl
41	456.5	70.1	637	1	US-08-235-838-16	Sequence 16, Appl
42	456.5	70.1	637	1	US-08-465-473B-16	Sequence 16, Appl
43	456	70.0	139	1	US-08-894-922A-5	Sequence 5, Appl
44	456	70.0	252	1	US-08-894-922A-14	Sequence 14, Appl
45	456	70.0	271	1	US-08-894-922A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-553-497A-12
Sequence 12, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUNSON, DETLEF
APPLICANT: ADAM, JAUDE
APPLICANT: MITYANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCES
APPLICANT: PIJUTAS, JAUDE
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-12

Query Match 75.7%; Score 493; DB 1; Length 119;
Best Local Similarity 79.5%; Pred. No. 7.6e-37;
Matches 97; Conservative 8; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVQLQQPVTSLVRPGASVMSCKASDYPFTNYWIMHWKORPGQGLEWIGVIDPSDTYPNY 60
DB 1 EVQLQQSGAEIVKPGASVYKLSCKASGYFTSYMMHWKORPGQGLEWIGVIDPSDTYNY 60
QY 61 NKKFKGKATLTIVVSSSTAYMQSLTSDSDSAVYYCARNGSDYYSS--GMDYWGQGTSTV 119
DB 61 NKKFKGKATLTIVDKSSSTAYMQSLTSDSDSAVYYCAR--SDYGSHPDYWGQGTIVTV 117
QY 120 SS 121
DB 118 SS 119

RESULT 2
US-10-092-246-12
Sequence 12, Application US/10092246
Patent No. 6501314

GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/092.246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 120
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-12

Query Match 74.3%; Score 483.5; DB 2; Length 120;

Best Local Similarity 76.6%; Pred. No. 5.4e-36;
Matches 95; Conservative 7; Mismatches 15; Indels 7; Gaps 2;

QY 1 QVQLQQPVTSLVRPGASVMSCKASDYPFTNYWIMHWKORPGQGLEWIGVIDPSDTYPNY 60
DB 1 EVQLQQSGAEIVKPGASVYKLSCKASGYFTSYMMHWKORPGQGLEWIGVIDPSDTYTY 60
QY 61 NKKFKGKATLTIVVSSSTAYMQSLTSDSDSAVYYCARNGSDYYSS--GMDYWGQGTSTV 117
DB 61 NKKFKGKATLTIVDKSSSTAYMQSLTSDSDSAVYYCAR--YYSRVSMIDYWGQGTSTV 116
QY 118 TVSS 121
DB 117 TVSS 120

RESULT 3
US-10-096-246A-12

Sequence 12, Application US/10096246A
Patent No. 6618748
GENERAL INFORMATION:
APPLICANT: Fulton, R. Elaine
APPLICANT: Nagata, Leslie
APPLICANT: Alvi, Azhar Z.
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
TITLE OF INVENTION: Monoclonal scFv Antibody Against Venezuelan Equine Encephalitis

TITLE OF INVENTION: Virus (VEE)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096.246A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 120
TYPE: PRT
ORGANISM: mouse
US-10-096-246A-12

Query Match 74.3%; Score 483.5; DB 2; Length 120;
Best Local Similarity 76.6%; Pred. No. 5.4e-36;
Matches 95; Conservative 7; Mismatches 15; Indels 7; Gaps 2;

QY 1 QVQLQQPVTSLVRPGASVMSCKASDYPFTNYWIMHWKORPGQGLEWIGVIDPSDTYPNY 60
DB 1 EVQLQQSGAEIVKPGASVYKLSCKASGYFTSYMMHWKORPGQGLEWIGVIDPSDTYTY 60
QY 61 NKKFKGKATLTIVVSSSTAYMQSLTSDSDSAVYYCARNGSDYYSS--GMDYWGQGTSTV 117
DB 61 NKKFKGKATLTIVDKSSSTAYMQSLTSDSDSAVYYCAR--YYSRVSMIDYWGQGTSTV 116
QY 118 TVSS 121
DB 117 TVSS 120

RESULT 4
US-08-553-497A-8
Sequence 8, Application US/08553497A
Patent No. 5844093

GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSEW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MULLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA


```

DE  VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN  Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6;
RA  Kozono Y., Kozono H., Azuma T.;
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB069912; BAB63928.1; -, mRNA.
DR  EMBL; AB069914; BAB63930.1; -, mRNA.
DR  PIR; S26744; S26744.
DR  HSSP; P01751; 1A6W.
DR  SMR; Q91V67; 1-129.
DR  Ensemble; ENSMUSG0000021155; Mus musculus.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  SMART; SM00406; IGV; 1_v.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 143
SQ  SEQUENCE 143 AA; 15775 MW; 91BC6012B44FEFEBF CRC64;

Query Match 75.5%; Score 491.5; DB 2; Length 143;
Best Local Similarity 78.5%; Pred. No. 3.8e-41;
Matches 95; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 OVQLQDPTELVKPGASVWLSCKASDYPFTNYWIHWKQRPQGQLEWIGVIDPSDTPYNY 60
DB 1 OVQLQDPGAEIVKPGTSVKLSCKASGYFTSYWMMHWKQRPQGQLEWIGVIDPSDTPYNY 60
QY 61 NKKFKGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDVYSGMDYWGQGSTVTVS 120
DB 61 NKKFKGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDVYSGMDYWGQGSTVTVS 117
QY 121 S 121
DB 118 S 118

RESULT 3
Q924Q1_MOUSE PRELIMINARY; PRT; 142 AA.
ID Q924Q1;
AC Q924Q1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=2499887;
RA Baccaia R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyclonal antibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=3135311;
RA Corbet S., Hirt M., Roth C., Theze J., Fougereau M., Schiff C.;

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RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BA9/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784 (1988).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; Pubmed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT "Both Igm and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZM) F1 mice.";
RL J. Exp. Med. 176:761-779 (1992).
DR EMBL; AB069913; BAB63929.1; -, mRNA.
DR PIR; F33932; F33932.
DR PIR; I28833; I28833.
DR PIR; PH0985; PH0985.
DR PIR; PH1155; PH1155.
DR PIR; PH1156; PH1156.
DR PIR; PH1157; PH1157.
DR PIR; PH1158; PH1158.
DR HSSP; P01751; 1A6W.
DR SMR; Q924Q1; 1-128.
DR Ensemble; ENSMUSG0000021155; Mus musculus.
DR MGI; MGI:3576502; AB069917.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 2A4265CE4EA4318B CRC64;

Query Match 74.8%; Score 487; DB 2; Length 142;
Best Local Similarity 78.5%; Pred. No. 1.1e-40;
Matches 95; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 OVQLQDPTELVKPGASVWLSCKASDYPFTNYWIHWKQRPQGQLEWIGVIDPSDTPYNY 60
DB 1 OVQLQDPGTELVKPGASVWLSCKASGYFTSYWMMHWKQRPQGQLEWIGVIDPSDTPYNY 60
QY 61 NKKFKGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDVYSGMDYWGQGSTVTVS 120
DB 61 NKKFKGKATLTVVSSSTAYWQLSLTSDSAVYYCARNGSDVYSGMDYWGQGSTVTVS 116
QY 121 S 121
DB 117 S 117

RESULT 4
O504M7_MOUSE PRELIMINARY; PRT; 616 AA.
ID O504M7;
AC O504M7;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCT; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Streusberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:22:00 / Search time 296.662 Seconds
(without alignments)
179.210 Million cell updates/sec

Title: US-10-524-134-2

Perfect score: 651
Sequence: 1 QVQLQQPVTBLVPGASVML.....SDYSGMDYWGQSTVTVSS 121

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	121	8 ADL00213	ADL00213 Human Fcg
2	502.5	77.2	122	8 ADH17833	ADH17833 Murine an
3	502.5	77.2	122	8 ADW11464	ADW11464 Murine an
4	502	77.1	119	8 ADP79380	ADP79380 Thyrocytop
5	493	75.7	124	8 ADP79384	ADP79384 Thyrocytop
6	492.5	75.7	119	2 AAR79863	AAR79863 Anti-EGFR
7	492.5	75.7	242	6 ABR62131	ABR62131 Single ch
8	491.5	75.5	242	8 ADT91207	ADT91207 Single ch
9	491.5	75.5	118	8 ADU39962	ADU39962 Antibody
10	489	75.1	119	8 AAW07436	AAW07436 Anti-DNA
11	489	75.1	140	2 AAW53815	AAW53815 Murine Ac
12	489	75.1	140	5 AAU1177	AAU1177 Mouse ant
13	489	75.1	144	2 AAW53816	AAW53816 Consensus
14	487	74.8	464	2 AAW83041	AAW83041 Anti-Fas
15	487	74.8	464	3 AAB14747	AAB14747 Mouse ant
16	487	74.8	464	3 AAW90897	AAW90897 Murine an
17	487	74.8	464	5 ABB74912	ABB74912 Humanised
18	482	74.0	466	5 ABB74866	ABB74866 Humanised
19	482	74.0	466	9 ADX39100	ADX39100 Mouse mon
20	482	74.0	466	9 ADX39137	ADX39137 Mouse mon
21	481	73.9	119	2 AAR79861	AAR79861 Anti-EGFR
22	477	73.3	137	2 AAW53818	AAW53818 Protein s
23	477	73.3	445	2 AAR76085	AAR76085 MAb 55.1
24	477	73.3	464	2 AAR76088	AAR76088 MAb 55.1

25	474.5	72.9	123	9 ADZ45377	ADZ45377 Murine fa
26	474	72.8	288	2 AAW82743	AAW82743 Fusion pr
27	474	72.8	673	2 AAW82742	AAW82742 Plasmid p
28	472	72.5	117	8 ADF77173	ADF77173 Anti-VAP-
29	472	72.5	119	8 ADG25806	ADG25806 Anti-CD30
30	472	72.5	119	8 ADG25812	ADG25812 Anti-CD30
31	472	72.5	143	8 ADI26636	ADI26636 Human ant
32	471.5	72.4	123	9 ADZ45369	ADZ45369 Murine fa
33	471	72.4	119	3 AAY92156	AAY92156 Murine 15
34	469	72.0	355	9 ADW77071	ADW77071 Heavy cha
35	468.5	72.0	123	9 ADZ45373	ADZ45373 Murine fa
36	468.5	72.0	123	9 ADZ45365	ADZ45365 Murine fa
37	467.5	71.8	118	9 ADZ21533	ADZ21533 Anti-Muc-
38	467.5	71.8	260	9 ADZ21542	ADZ21542 Anti-Muc-
39	466.5	71.7	467	8 ADQ14477	ADQ14477 Mouse ant
40	466	71.6	119	2 AAK00835	AAK00835 Variable
41	466	71.6	138	2 AAW50218	AAW50218 Amino aci
42	464.5	71.4	121	9 ADZ45353	ADZ45353 Murine fa
43	464.5	71.4	122	2 AAR84555	AAR84555 B-cell ly
44	464.5	71.4	309	4 AAB70841	SNV-envy 1
45	463	71.1	111	2 AAW04586	AAW04586 Anti-DNA

ALIGNMENTS

RESULT 1	ADL00213	standard; protein; 121 AA.
ID	ADL00213	
AC	ADL00213	
XX	20-MAY-2004	(first entry)
DE	Human FcgammaRIIB antibody heavy chain.	
XX	Cytostatic; antirheumatic; antiarthritic; antipsoriatic; dermatological;	
KW	immunosuppressive; antineoplastic; antitumor; antiallergic;	
KW	immunoregulatory; nephrotoxic; ophthalmological;	
KW	B cell receptor-mediated signaling modulator;	
KW	Fc gamma RI-induced mast cell activation modulator;	
KW	B cell activation modulator; B cell proliferation modulator;	
KW	antibody production modulator; intracellular calcium influx modulator;	
KW	vacuole composition efficiency enhancer; gene therapy; FcgammaRIIB; cancer;	
KW	breast cancer; ovarian cancer; prostate cancer; cervical cancer;	
KW	pancreatic cancer; chemotherapy; immunotherapy; radiation therapy;	
KW	hormonal therapy; autoimmune disorder; rheumatoid arthritis;	
KW	psoriatic arthritis; ankylosing spondylitis; Riecher's Syndrome;	
KW	psoriasis; lupus erythematosus; IGE-mediated allergic disorder; asthma;	
KW	allergic rhinitis; gastrointestinal allergy; eosinophilia;	
KW	conjunctivitis; glomerular nephritis; autoimmune disease; vaccine;	
KW	B cell malignancy; non-Hodgkin's lymphoma; solid tumour;	
KW	fragment of crystallisation gamma receptor IIB; antibody heavy chain;	
XX	human.	
OS	Homo sapiens.	
XX	WO2004016750-A2.	
PN	26-FEB-2004.	
XX	14-AUG-2003; 2003WO-US025399.	
PF	14-AUG-2002; 2002US-0403266P.	
XX	(MACR-) MACROGENICS INC.	
PA	Koenig S, Veri M;	
PI	WPI, 2004-203783/19.	
DR	N-PSDB; ADL00212.	
XX	Novel isolated antibody or its fragment useful for treating diseases	

PT e.g., cancer, that specifically binds native FcgammaRIIb with greater
PT affinity than antibody or its fragment that binds native FcgammaRIIA.
XX
PS Disclosure; SEQ ID NO 2; 174pp; English.

CC The invention describes an isolated antibody or its fragment (I) that
CC specifically binds native FcgammaRIIb. (I) is useful for treating cancer
CC (e.g., breast, ovarian, prostate, cervical or pancreatic cancer) in a
CC patient (e.g., human) having cancer with specific cancer antigen which
CC involves administering a first antibody or its fragment which is (I) and
CC a second antibody that specifically binds the cancer antigen and is
CC cytotoxic. The above method further involves administration of one or
CC more additional cancer therapies such as chemotherapy, immunotherapy,
CC radiation therapy, hormonal therapy, or surgery. (I) is useful for
CC treating an autoimmune disorder e.g., rheumatoid arthritis, psoriatic
CC arthritis, ankylosing spondylitis, Reiter's Syndrome, psoriasis, or lupus
CC erythematosus. The above method further involves administering to the
CC patient a therapeutically effective amount of one or more anti-
CC inflammatory agents or immunomodulatory agents e.g., small organic
CC molecule such as methotrexate or corticosteroid. The anti-inflammatory
CC agent is a non-steroidal anti-inflammatory drug e.g., aspirin or
CC ketoprofen. (I) is also useful for: treating IGE-mediated allergic
CC disorder such as asthma, allergic rhinitis, gastrointestinal allergies,
CC eosinophilia, conjunctivitis, or glomerular nephritis; enhancing an
CC antibody mediated cytotoxic effect in a subject; diagnosing an autoimmune
CC disease in a subject; enhancing an immune response to a vaccine
CC composition in a subject; treating a B cell malignancy (e.g., non-
CC Hodgkin's lymphoma); treating a disease in a patient; treating a solid
CC tumour in a patient; and treating cancer in a patient. (I) has an altered
CC affinity for an FcgammaRII. (I) antibody binds FcgammaRIIA with a higher
CC affinity than a comparable antibody comprising a wild-type Fc region
CC binds FcgammaRIIA. (I) has an enhanced antibody mediated effector
CC function relative to a comparable antibody comprising a wild-type Fc
CC region. This is the amino acid sequence of human fragment of
CC crystallization gamma receptor IIB (FcgammaRIIb) antibody heavy chain.
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 651; DB 8; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.2e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQGPVTELVKPGASVMTLSCKASDYPFTNWMHWKQRPQGQLEWIGVLDPSDTPYNY 60
DB 1 QVQLQGPVTELVKPGASVMTLSCKASDYPFTNWMHWKQRPQGQLEWIGVLDPSDTPYNY 60
QY 61 NKKFKGKATLTVVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVVS 120
DB 61 NKKFKGKATLTVVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGTSTVVS 120
QY 121 S 121
DB 121 S 121

RESULT 2
ADH17833
ID ADH17833 standard; protein; 122 AA.

AC ADH17833;
XX
DT 11-MAR-2004 (first entry)
XX
DE Murine antibody 1fbi heavy chain variable region protein.

KW antibody EM164; insulin-like growth factor-I receptor; IGF-IR antagonist;
KW breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
KW prostate; lung; synovial carcinoma; pancreatic; murine; mouse;
XX heavy chain variable region; 1fbi.

OS Mus sp.
XX
PN WO2003106621-A2.

XX
PD 24-DEC-2003.
XX
PF 12-JUN-2003; 2003MO-US016211.
XX
PR 14-JUN-2002; 2002US-00170390.

XX (IMMU-) IMMUNOGEN INC.
XX
PI Singh R, Tavares DJ, Dagdigian NE;
XX
DR WPI; 2004-082172/08.

XX Novel murine antibody EM164 or antibody fragment that specifically binds
PT to insulin-like growth factor-I-receptor useful for treating breast
PT cancer, colon cancer, lung cancer, prostate cancer.

XX Example 2; SEQ ID NO 73; 155pp; English.

CC The invention relates to a novel murine antibody EM164 or antibody
CC fragment that specifically binds to insulin-like growth factor-I receptor
CC (IGF-IR) where the antibody is an antagonist of the receptor, is
CC substantially devoid of agonist activity toward the receptor and is
CC capable of inhibiting the growth of a cancer cell by greater than 80% in
CC the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
CC The antibody of the invention may be useful for diagnosing or treating a
CC patient having a cancer selected from breast cancer, colon cancer,
CC ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
CC cancer, synovial carcinoma and pancreatic cancer. The current sequence is
CC that of the murine anti-IGF-IR antibody EM164-related protein of the
CC invention.

XX
SQ Sequence 122 AA;
Query Match 77.2%; Score 502.5; DB 8; Length 122;
Best Local Similarity 78.6%; Pred. No. 1.5e-34;
Matches 99; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

QY 1 QVQLQGPVTELVKPGASVMTLSCKASDYPFTNWMHWKQRPQGQLEWIGVLDPSDTPYNY 60
DB 1 QVQLQGPVTELVKPGASVMTLSCKASDYPFTNWMHWKQRPQGQLEWIGVLDPSDTPYNY 60
QY 61 NKKFKGKATLTVVVSSSTAYWQLSLTSDSAVYYCARNGSDYYSGMDYWGQGT 115
DB 61 NKKFKGKATLTVDKSSSTAYWQLSLTSDSAVYYCA----SLYYGTSTYGVLDYWGQGT 116
QY 116 SVTVSS 121
DB 117 SVTVSS 122

RESULT 3
ADW11464
ID ADW11464 standard; protein; 122 AA.

AC ADW11464;
XX
DT 24-MAR-2005 (first entry)
XX
DE Murine anti-IGF I receptor antibody EM164 VH-homologous 1fbi protein.

XX antibody; cytostatic; cancer; neoplasm; breast tumor; colon tumor;
KW uterine cervix tumor; prostatic cancer; lung tumor; pancreas tumor;
KW ovary tumor; carcinoma; osteosarcoma; melanoma; nervous system tumor;
XX gene therapy; heavy chain variable region.

OS Unidentified.
XX
PN US2004265307-A1.

XX 30-DEC-2004.
PD
PF 08-DEC-2003; 2003US-00729441.

